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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Papayannopoulou, Thalia (USA only)
Board of Regents, U.
Washington (except USA)

(ii) TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
CELLS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: c/o FISH & NEAVE
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(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10020

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/977,702
(B) FILING DATE: 13-NOV-1992

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Haley Jr., James F.
(B) REGISTRATION NUMBER: 27,794
(C) REFERENCE/DOCKET NUMBER: B173CIP

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 596-9000
(B) TELEFAX: (212) 596-9090

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GTCAAAGTGC AGCAGTCTGG GGCAGAGCTT GTGAAGCCAG GGGCCTCAGT CAAGTTGTCC 60
TGCACAGCTT CTGGCTTCAA CATTAAAGAC ACCTATATGC ACTGGGTGAA GCAGAGGCCT 120
GAACAGGGCC TGGAGTGGAT TGAAGGATT GATCCTGCGA GTGGCGATAC TAAATATGAC 180
CCGAAGTTCC AGGTCAAGGC CACTATTACA GCGGACACGT CCTCCAACAC AGCCTGGCTG 240
CAGCTCAGCA GCCTGACATC TGAGGACACT GCCGTCTACT ACTGTGCAGA CGGAATGTGG 300
GTATCAACGG GATATGCTCT GGAATTCTGG GGCCAAGGGA CCACGGTCAC CGTCTCTCTCA 360

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGTATTGTGA TGACCCAGAC TCCCAAATTC CTGCTTGTTT CAGCAGGAGA CAGGGTTACC 60
ATAACCTGCA AGGCCAGTCA GAGTGTGACT AATGATGTAG CTTGGTACCA ACAGAAGCCA 120
GGGCAGTCTC CTAACTGCT GATATATTAT GCATCCAATC GCTACACTGG AGTCCCTGAT 180
CGCTTCACTG GCAGTGGATA TGGGACGGAT TTCACCTTCA CCATCAGCAC TGTGCAGGCT 240
GAAGACCTGG CAGTTTATTT CTGTCAGCAG GATTATAGCT CTCCGTACAC GTTCGGAGGG 300
GGGACCAAGC TGGAGATC 318

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid

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37

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..57

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 58..429

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..429

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "pMDR1019 insert: Stage 1
heavy chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | |
|---|-----|
| ATG GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCA CCA GGT | 48 |
| Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly | |
| -19 -15 -10 -5 | |
| GCC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA | 96 |
| Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg | |
| 1 5 10 | |
| CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GTG TCT GGC TTC AAC ATT | 144 |
| Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Asn Ile | |
| 15 20 25 | |
| AAA GAC ACC TAT ATG CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT | 192 |
| Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu | |
| 30 35 40 45 | |
| GAG TGG ATT GGA AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC | 240 |
| Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp | |
| 50 55 60 | |
| CCG AAG TTC CAG GTC AGA GTG ACA ATG CTG GTA GAC ACC AGC AAG AAC | 288 |
| Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn | |
| 65 70 75 | |
| CAG TTC AGC CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC | 336 |
| Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val | |

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38

80 85 90

TAT TAT TGT GCA GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC 384

Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
95 100 105

TTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GAG TCC 429

Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
110 115 120

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
-19 -15 -10 -5

Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
1 5 10

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Asn Ile
15 20 25

Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
30 35 40 45

Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
50 55 60

Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn
65 70 75

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
80 85 90

Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
95 100 105

Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
110 115 120

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs

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39

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..57

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 58..384

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..384

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /note= "pBag190 insert: VK1 (DQL)
 light chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|---|-----|
| ATG GGT TGG TCC TGC ATC ATC CTG TTC CTG GTT GCT ACC GCT ACC GGT | 48 |
| Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly | |
| -19 -15 -10 -5 | |
| GTT CAC TCC GAC ATC CAG CTG ACC CAG AGC CCA AGC AGC CTG AGC GCC | 96 |
| Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala | |
| 1 5 10 | |
| AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AGT GTG | 144 |
| Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val | |
| 15 20 25 | |
| ACT AAT GAT GTA GCT TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG | 192 |
| Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys | |
| 30 35 40 45 | |
| CTG CTG ATC TAC TAT GCA TCC AAT CGC TAC ACT GGT GTG CCA AGC AGA | 240 |
| Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg | |
| 50 55 60 | |
| TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC | 288 |
| Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser | |
| 65 70 75 | |
| CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAG GAT TAT AGC | 336 |

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$$- \overset{39}{\cancel{40}} \bar{0}$$

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
80 85 90

TCT CCG TAC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT AAG 384

Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
95 100 105

TG 386

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
15 20 25

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asn | Asp | Val | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys |
| 30 | | | | | 35 | | | | | 40 | | | | | 45 |

Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
80 85 90

Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
95 100 105

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

HD

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41

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..57

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 58..429

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..429

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "pBAG195 insert: AS heavy
chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | |
|---|-----|
| ATG GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCA CCA GGT | 48 |
| Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly | |
| -19 -15 -10 -5 | |
| GCC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA | 96 |
| Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg | |
| 1 5 10 | |
| CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GCG TCT GGC TTC AAC ATT | 144 |
| Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile | |
| 15 20 25 | |
| AAA GAC ACC TAT ATG CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT | 192 |
| Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu | |
| 30 35 40 45 | |
| GAG TGG ATT GGA AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC | 240 |
| Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp | |
| 50 55 60 | |
| CCG AAG TTC CAG GTC AGA GTG ACA ATG CTG GTA GAC ACC AGC AGC AAC | 288 |
| Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn | |
| 65 70 75 | |
| CAG TTC AGC CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC | 336 |
| Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val | |
| 80 85 90 | |

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TAT TAT TGT GCA GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC 384
 Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
 95 100 105
 TTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GAG TCC 429
 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
 110 115 120

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
 -19 -15 -10 -5
 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
 1 5 10
 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
 15 20 25
 Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
 30 35 40 45
 Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
 50 55 60
 Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
 65 70 75
 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 80 85 90
 Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
 95 100 105
 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
 110 115 120

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

42

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43

(A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..57

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 58..384

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..384

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /note= "pBAG198 insert VK2 (SVMDY)
 light chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | |
|---|-----|
| ATG GGT TGG TCC TGC ATC ATC CTG TTC CTG GTT GCT ACC GCT ACC GGT | 48 |
| Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly | |
| -19 -15 -10 -5 | |
| GTC CAC TCC AGC ATC GTG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC | 96 |
| Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala | |
| 1 5 10 | |
| AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AGT GTG | 144 |
| Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val | |
| 15 20 25 | |
| ACT AAT GAT GTA GCT TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG | 192 |
| Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys | |
| 30 35 40 45 | |
| CTG CTG ATC TAC TAT GCA TCC AAT CGC TAC ACT GGT GTG CCA GAT AGA | 240 |
| Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg | |
| 50 55 60 | |
| TTC AGC GGT AGC GGT TAT GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC | 288 |
| Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser | |
| 65 70 75 | |

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CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAG GAT TAT AGC 336
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
 80 85 90
 TCT CCG TAC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT AAG 384
 Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
 95 100 105
 TG 386

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 -19 -15 -10 -5
 Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
 1 5 10
 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
 15 20 25
 Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 30 35 40 45
 Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
 50 55 60
 Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
 65 70 75
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
 80 85 90
 Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
 95 100 105

H4